09/935377

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 NEWS  2  Jan 25  BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29  FSTA has been reloaded and moves to weekly updates
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                  frequency
 NEWS  5  Feb 19  Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08  Gene Names now available in BIOSIS
 NEWS  7  Mar 22  TOXLIT no longer available
 NEWS  8  Mar 22  TRCTHERMO no longer available
 NEWS  9  Mar 28  US Provisional Priorities searched with P in CA/CAplus
                  and USPATFULL
 NEWS 10  Mar 28  LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02  PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08  "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09  ZDB will be removed from STN
 NEWS 15  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS 19  May 31  PCTFULL to be reloaded.  File temporarily unavailable.

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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                                                       ENTRY    SESSION
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=> s zauderer M?/au
L1          127 ZAUDERER M?/AU

=> s l1 and ctl?
L2            4 L1 AND CTL?

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3            4 DUP REM L2 (0 DUPLICATES REMOVED)

=> dis l3 1-4 ibib abs

L3   ANSWER 1 OF 4  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2002:123514  CAPLUS
DOCUMENT NUMBER:          136:182454
TITLE:                    Methods for identifying and producing antigens for
                          treating cancer and infection
INVENTOR(S):              Zauderer, Maurice
PATENT ASSIGNEE(S):       University of Rochester, USA
SOURCE:                   U.S. Pat. Appl. Publ., 54 pp., Division of U.S. Ser.
                          No. 935,377.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.          KIND  DATE           APPLICATION NO.  DATE
     ----------------    ----  --------       ---------------  --------
     US 2002018785       A1    20020214       US 2001-822250   20010402
PRIORITY APPLN. INFO.:                      US 1997-935377   A3 19970922
AB   The present invention relates to novel methods for the identification of
     antigens recognized by cytotoxic T cells (CTLs) and specific for
     human tumors, cancers, and infected cells, and the use of such antigens in
     immunogenic compns. or vaccines to induce regression of tumors, cancers,
```

or infections in mammals, including humans. The invention encompasses methods for induction and isolation of cytotoxic T cells specific for human tumors, cancers and infected cells, and for improved selection of genes that encode the target antigens recognized by these specific T cells. The invention also relates to differential display methods that improve resoln. of, and that reduce the frequency of false positives of DNA fragments that are differentially expressed in tumorous, cancerous, or infected tissues vs. normal tissues. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer, or infected cell-specific antigens.

L3 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:780722 CAPLUS
DOCUMENT NUMBER: 135:348863
TITLE: Targeted vaccine delivery systems
INVENTOR(S): **Zauderer, Maurice**; Smith, Ernest S.
PATENT ASSIGNEE(S): University of Rochester, USA
SOURCE: PCT Int. Appl., 167 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001078768	A2	20011025	WO 2001-US11912	20010412

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-196472P P 20000412
AB The present invention is directed to a novel targeted vaccine delivery system, comprising one or more MHC-peptide complexes linked to an antibody which is specific for a cell surface marker. The complexes of the invention are useful for treating and/or preventing cancer, infectious diseases, autoimmune diseases, and/or allergies.

L3 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:747830 CAPLUS
DOCUMENT NUMBER: 135:314437
TITLE: Identification and characterization of a novel gene C35 differentially expressed in breast and bladder cancer and cancer immunotherapy thereof
INVENTOR(S): **Zauderer, Maurice**; Evans, Elizabeth E.; Borrello, Melinda A.
PATENT ASSIGNEE(S): University of Rochester, USA
SOURCE: PCT Int. Appl., 331 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001074859	A2	20011011	WO 2001-US10855	20010404
WO 2001074859	A3	20020328		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-194463P P 20000404
AB The present invention relates to a novel human gene that is differentially expressed in human carcinoma. More specifically, the present invention relates to a polynucleotide encoding a novel human polypeptide named C35 that is overexpressed in human breast and bladder carcinoma. The full-length gene aligns on human chromosome 17q12 and mouse chromosome 11 and encodes a novel 115 amino acid-membrane protein of unknown function. A monoclonal antibody, 2C3, has been selected which can detect the C35 surface expression by flow cytometric anal. and is shown to inhibit the growth of C35 overexpressed tumor cell lines. In addn., human cytotoxic T lymphocytes (**CTL**) have been generated in vitro that specifically lyse C35+ breast and bladder tumors. These T cells are strongly stimulated to secrete interferon .alpha. and interferon .gamma. by the breast lines that expressed both C35 and HLA-A2, indicate that there is at least one C35 Class I epitope is HLA-A2 restricted. Overexpression of C35 in tumors of different individuals and the ability to induce humoral and cellular immune responses make C35 a promising candidate for immunotherapy.

L3 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:335539 CAPLUS
DOCUMENT NUMBER: 133:1478
TITLE: Methods for identifying genes of tumor specific antigens recognized by cytotoxic T cells and cancer vaccines based thereon
INVENTOR(S): **Zauderer, Maurice**
PATENT ASSIGNEE(S): University of Rochester, USA
SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000028016	A1	20000518	WO 1998-US24029	19981110

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,

NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9913977 A1 20000529 AU 1999-13977 19981110
EP 1137769 A1 20011004 EP 1998-957808 19981110
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, FI
PRIORITY APPLN. INFO.: WO 1998-US24029 A 19981110
AB The present invention relates to novel methods for the identification of genes of antigens recognized by cytotoxic T cells (CTLs) and specific for human tumors, cancers, and infected cells, and the use of genes of such antigens in immunogenic compns. or vaccines to induce regression of tumors, cancers, or infections in mammals, including humans. The invention also relates to differential display methods that improve resoln. of, and that reduce the frequency of false positives of DNA fragments that are differentially expressed in tumorous, cancerous, or infected tissues vs. normal tissues. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer, or infected cell-specific antigens.
REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s librar?
L4 192122 LIBRAR?

=> s l4 (P) CTL
L5 366 L4 (P) CTL

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SYSTEM LIMITS EXCEEDED - SEARCH ENDED
75% OF LIMIT FOR TOTAL ANSWERS REACHED
3 FILES SEARCHED...
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'19970922' NOT A VALID FIELD CODE
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SEARCH ENDED BY USER
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'19970922' NOT A VALID FIELD CODE
3 FILES SEARCHED...
L6 146 L5 AND PD<19970922

=> s l6 (P) (epitop? or peptid?)
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L22 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L23 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L24 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L25 (P) '
L7 89 L6 (P) (EPITOP? OR PEPTID?)

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FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 07:13:57 ON 03 JUN 2002
L1 127 S ZAUDERER M?/AU
L2 4 S L1 AND CTL?
L3 4 DUP REM L2 (0 DUPLICATES REMOVED)
L4 192122 S LIBRAR?
L5 366 S L4 (P) CTL
L6 146 S L5 AND PD<19970922
L7 89 S L6 (P) (EPITOP? OR PEPTID?)

=> s l7 and mhc
L8 39 L7 AND MHC

=> dis l8 1-39 ibib abs

L8 ANSWER 1 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:462415 CAPLUS
DOCUMENT NUMBER: 127:189254
TITLE: Antigen processing by proteasomes: insights into the molecular basis of crypticity
AUTHOR(S): Djaballah, Hakim
CORPORATE SOURCE: MRC Transplantation Biology Group, Royal Postgraduate Medical School, Hammersmith Hospital, London, W12 0NN, UK
SOURCE: Mol. Biol. Rep. (1997), 24(1-2), 63-67
CODEN: MLBRBU; ISSN: 0301-4851
PUBLISHER: Kluwer
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 44 refs. Eight to eleven amino acid residues are the sizes of predominant **peptides** found to be assocd. with **MHC** class I mols. Proteasomes have been implicated in antigen processing and generation of such **peptides**. Advanced methodologies in **peptide** elution together with sequence detn. have led to the characterization of **MHC** class I binding motifs. More recently, screening of random **peptide** phage display **libraries** and synthetic combinatorial **peptide libraries** have

also been successfully used. This has led to the development and use of predictive algorithms to screen antigens for potential cytotoxic T-lymphocyte (**CTL**) **epitopes**. Not all predicted **epitopes** will be generated in vivo and the emerging picture suggests differential presentation of predicted **CTL epitopes** ranging from cryptic to immunodominant. Antigen processing by proteasomes is discussed, a hypothesis that the mol. basis of immunogenicity can be a function of proteasomal processing is advanced. This may explain how pathogens and tumors are able to escape immunosurveillance by altering sequences required by proteasomes for **epitope** generation.

L8 ANSWER 2 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:147340 CAPLUS
DOCUMENT NUMBER: 126:198410
TITLE: Cytotoxic T cell induction with ratchet **peptide** libraries
AUTHOR(S): Kuebler, Peter J.; Nixon, Douglas F.
CORPORATE SOURCE: United Biomedical, Inc., Hauppauge, NY, 11788, USA
SOURCE: Vaccine (**1996**), 14(17/18), 1664-1670
CODEN: VACCDE; ISSN: 0264-410X
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Immunization with synthetic **peptides** are used to induce cytotoxic T cell (**CTL**) responses in vivo. However, **CTL peptide** vaccines require the use of multiple **peptides** to overcome genetic diversity assocd. with **MHC** restriction, and prior **epitope** identification from the chosen protein template. The authors describe here a method whereby all nonamer sequences from a longer template can be synthesized simultaneously in a ratchet **peptide library** (RPL) covering all potential **epitopes** within a protein. The authors synthesized an RPL based on a template sequence from the Plasmodium berghei circumsporozoite (CS) protein (CSRPL). Using a lipopeptide formulation the authors immunized mice i.p. with the CSRPL and elicited CS specific **CTL**, which recognized the CS252-260 H-2Kd restricted **CTL epitope**.

L8 ANSWER 3 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:111450 CAPLUS
DOCUMENT NUMBER: 126:184804
TITLE: Identification of tyrosinase-related protein 2 as a tumor rejection antigen for the B16 melanoma
AUTHOR(S): bloom, Matthew b.; Perry-Lalley, Donna; Robbins, Paul F.; Li, Yong; El-Gamil, Mona; Rosenberg, Steven A.; Yang, James C.
CORPORATE SOURCE: Natl. Cancer Inst., Natl. Inst. Health, Bethesda, MD, 20892, USA
SOURCE: J. Exp. Med. (**1997**), 185(3), 453-459
CODEN: JEMEAV; ISSN: 0022-1007
PUBLISHER: Rockefeller University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Recently, major advances have been made in the identification of antigens from human melanoma which are recognized by T cells. In spite of this, little is known about the optimal ways to use these antigens to treat patients with cancer, Progress in this area is likely to require accurate preclin. animal models, but the availability of such models has lagged behind developments in human tumor immunol. Whereas many of the identified human melanoma antigens are normal tissue differentiation proteins, analogous murine tumor antigens have not yet been identified. In this paper we identify a normal tissue differentiation antigen, tyrosinase-related protein 2 (TRP-2), expressed by the murine B16 melanoma which was found by screening a cDNA **library** from B16 with tumor-reactive cytotoxic T lymphocytes (**CTL**). A **peptide** conforming to the predicted **MHC** class I H2-Kb binding motif, TRP-2181-188, was identified a the major reactive **epitope** within TRP-2 recognized by these anti-B16 **CTLs**. By site-directed mutagenesis, it was shown that alteration of this **epitope** eliminated recognition of TRP-2. It was further demonstrated that the **CTL** line obtained from splenocytes by repeated stimulation in vitro with this **peptide** could recognize B16 tumor and was therapeutic against 3-d-old established pulmonary metastases. The use of TRP-2 in a preclin. model of tumor immunotherapy may be helpful in suggesting optimal vaccination strategies for cancer therapy in patients.

L8 ANSWER 4 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:72877 CAPLUS
DOCUMENT NUMBER: 126:143035
TITLE: Identification of potential CTL **epitopes** of bovine RSV using allele-specific **peptide** motifs from bovine **MHC** class I molecules
AUTHOR(S): Gaddum, R. M.; Ellis, S. A.; Willis, A. C.; Cook, R. S.; Staines, K. A.; Thomas, L. H.; Taylor, G.
CORPORATE SOURCE: Inst. Animal Health, Compton, Newbury, RG20 7NN, UK
SOURCE: Vet. Immunol. Immunopathol. (**1996**), 54(1-4), 211-219
CODEN: VIIMDS; ISSN: 0165-2427
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Respiratory syncytial virus (RSV) is a major cause of lower respiratory tract infection in young infants and housed calves. Depletion of CD8+ lymphocytes from calves inhibited their ability to clear the virus from the nasopharynx and lungs. To study these cells further, a cytotoxic T lymphocyte (**CTL**) assay was established. **CTL** could be demonstrated in the peripheral blood of gnotobiotic calves 7-10 days post infection (p.i.) with RSV and in lungs 10 days p.i. This response was both **MHC**-restricted and virus-specific. Following sepn. of the lung lymphocytes by magnetic activated cell sorting, it was shown that the cytolytic activity was mediated by cells of the CD8+ phenotype. To identify **epitopes** recognized by bovine **CTL**, the consensus motifs from **MHC** class I alleles were identified. CDNA **libraries** were constructed and screened for full length class I sequences. The isolated cDNA clones were then transfected into mouse P815 cells and the expressed product immunopptd. and matched with a serol. specificity. The bovine **MHC** class I mols. were isolated from lysed transfected cells by affinity chromatog., using a monoclonal antibody specific for bovine **MHC** class I, and bound **peptides** were sepd. by reverse-phase HPLC. Anal. of the protein sequences of bovine RSV for the defined motifs has identified potential **CTL epitopes**.

L8 ANSWER 5 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:563443 CAPLUS
DOCUMENT NUMBER: 125:219603
TITLE: **Peptide** ratchet **libraries** for **CTL**-inducing vaccines and therapeutics
INVENTOR(S): Kuebler, Peter J.; Nixon, Douglas F.
PATENT ASSIGNEE(S): United Biomedical, Inc., USA
SOURCE: PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9622067	A2	19960725	WO 1995-US16290	19951215 <--
WO 9622067	A3	19961128		
W: AU, CA, FI, JP, NO				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9658497	A1	19960807	AU 1996-58497	19951215 <--
PRIORITY APPLN. INFO.:			US 1994-366332	19941227
			WO 1995-US16290	19951215

AB The present invention relates to ratchet **libraries** composed of related **peptides** synthesized simultaneously in a single **peptide** synthesis. Ratchet **libraries** are derived from a longer template **peptide** by sequentially "ratcheting" the template sequence into the shorter ratchet length and are used for cytotoxic T lymphocyte (**CTL**) induction or stimulation if the **CTL epitope** is known. If the **CTL epitope** is unknown, then the ratchet **library** can be used for identification of **CTL epitopes**. The ratchet **libraries** can be prepd. from any protein sequence to which an immune **CTL** response is desired and can be formulated for delivery as a vaccine or therapeutic for the treatment or prevention of disease or malignancy. For example, a ratchet **library** can be used in the prevention and treatment of infectious or malignant diseases including HIV, influenza, malaria, breast, ovarian, lung and colon cancers.

L8 ANSWER 6 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:422019 CAPLUS
DOCUMENT NUMBER: 125:84043
TITLE: Use of combinatorial **peptide** libraries to construct functional mimics of tumor **epitopes** recognized by **MHC** class I-restricted cytolytic T lymphocytes
AUTHOR(S): Blake, James; Johnston, Janet V.; Hellstroem, Karl Erik; Marquardt, Hans; Chen, Lieping
CORPORATE SOURCE: Bristol-Myers Squibb Pharmaceutical Res. Inst., Seattle, WA, 98121, USA
SOURCE: J. Exp. Med. (**1996**), 184(1), 121-130
CODEN: JEMEAV; ISSN: 0022-1007
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Identification of cytolytic T lymphocyte (**CTL**) **epitopes** presented by major histocompatibility complex (**MHC**) class I mols. on tumor cells is crit. for the design of active immunotherapy. We describe the use of combinatorial **peptide libraries** with defined amino acids in two **MHC** anchor positions to search for **epitopes** that are recognized by H-2Db- and Kb-restricted **CTL** specific for the mouse lymphoma EL4. An iterative strategy was used for screening **libraries** in which 16 amino acids were divided into 3 groups and 3 subgroups: .alpha.(AL, VT, FY); .beta.(GS, P, DE); .gamma.(KR, H, NQ). The proportions of each group and subgroup at individual **peptide** positions were changed in the **library** synthesis, and the effect of these changes on **CTL** activity was measured in a sensitive RMA-S cell assay. A single H-2Db **epitope** mimic was deduced from the original **library** that contained >2 .times. 108 potential **peptides** and was at least 9 logs more potent than the original **library**. Immunization of syngeneic mice with this **peptide** elicited **CTL** that lysed EL4 cells as well as RMA-S cells pulsed with **peptides** isolated from Db mols. of EL4 cells, indicating functional similarity between the mimicking **peptide** and the naturally processed **CTL epitope**. Furthermore, adoptive transfer of such a **CTL** line had a therapeutic effect in mice with EL4 established as an ascites tumor. Two H-2Kb-restricted **epitope** mimics of the same tumor were also identified. Our method represents a novel approach for the construction of **MHC** class I-restricted targets that can serve a immunogens for active immunotherapy of cancer.

L8 ANSWER 7 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:408481 CAPLUS
DOCUMENT NUMBER: 125:84015
TITLE: Self-**MHC**-restricted **peptides** recognized by an alloreactive T lymphocyte clone
AUTHOR(S): Udaka, Keiko; Wiesmueller, Karl-Heinz; Kienle, Stefan; Jung, Guenther; Walden, Peter
CORPORATE SOURCE: Max Planck Inst. Biology, Immunogenetics Section, Tuebingen, Germany
SOURCE: J. Immunol. (**1996**), 157(2), 670-678
CODEN: JOIMA3; ISSN: 0022-1767
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Alloreactive T lymphocytes are readily detected in unprimed animals although they have never encountered the alloantigen before. This well-established phenomenon is usually explained with the assumption that a self-**MHC** mol. complexed with a defined **peptide** resembles the allo-**MHC** mol. with another **peptide** and induces the corresponding T cell specificities. Here, for the first time and in support of this hypothesis, self-**MHC**-restricted **peptides** are described for a T cell clone that was induced with allo-**MHC**. The allo-**MHC**-specific **CTL** clone 2C was derived from a H-2b mouse and recognizes H-2Ld complexed with the naturally occurring endogenous **peptide** LSPFPFDL. H-2Kb was shown to be involved in pos. selection of its TCR, and **peptides** assocd. with this **MHC** mol. are implicated in the process. To identify such **peptides**, positional scanning with random **peptide libraries** combined with an iterative approach was employed. Several active **peptides** were found and the most

efficient, SIYRYYGL, was chosen for further studies. Recognition by 2C of the two **MHC-peptide** adducts H-2Ld + LSPFPFDL and H-2Kb + SIYRYYGL is mediated by the same TCR and appears to be similarly efficient as concluded from inhibition expts. with an Id-specific Ab. **CTLs** from SIYRYYGL-primed H-2b mice respond to H-2Ld + LSPFPFDL. This reciprocal cross-reactivity suggests that structural features are shared by the two **MHC-peptide** complexes.

L8 ANSWER 8 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:282493 CAPLUS
DOCUMENT NUMBER: 124:340313
TITLE: Specificity and degeneracy of minor histocompatibility antigen-specific **MHC**-restricted **CTL**
AUTHOR(S): Gundlach, Bjoern R.; Wiesmueller, Karl-Heinz; Junt, Tobias; Kienle, Stefan; Jung, Guenther; Walden, Peter
CORPORATE SOURCE: Section Immunogenet., Max Planck Inst. Biol., Tubingen, Germany
SOURCE: J. Immunol. (1996), 156(10), 3645-3651
CODEN: JOIMA3; ISSN: 0022-1767
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Random **peptide libraries** were employed to investigate the specificity of Ag recognition by H-3-specific, H-2Kb-restricted **CTL** clones. The **peptide libraries** consist of octapeptides with one defined sequence position and mixts. of 19 amino acids (all proteinogenic amino acids except for cysteine) in the remaining seven sequence positions. The complete set of 152 **peptide libraries** includes all octapeptides possible with these amino acids. Responses of the **CTL** clones to these **peptide libraries** reveal patterns of preferred **epitope** amino acids. Depending on the **CTL** clone tested, varying nos. of different amino acids were identified for the different sequence positions indicating degeneracy of Ag recognition. Sequences for synthetic **epitopes** active at low pM concns. could be deduced from these patterns. They confirm that TCRs of **CTL** clones do not exhibit specificity for unique ligand structures but rather can interact with sets of ligands. The sequences of **peptides** recognized by a single clone exhibit great sequence heterogeneity.

L8 ANSWER 9 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:11929 CAPLUS
DOCUMENT NUMBER: 124:53176
TITLE: Increased **peptide** promiscuity provides a rationale for the lack of N regions in the neonatal T cell repertoire
AUTHOR(S): Gavin, Marc A.; Bevan, Michael J.
CORPORATE SOURCE: Dept. Immunology, Univ. Washington, Seattle, WA, 98195-7370, USA
SOURCE: Immunity (**1995**), 3(6), 793-800
CODEN: IUNIEH; ISSN: 1074-7613
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Making use of mice deficient for terminal deoxynucleotidyl transferase (TdT) expression and a random **peptide library**, the authors have examd. the diversity and **peptide** specificity of the neonatal T cell repertoire specific for a single H-2Db-restricted **peptide**. Consistent with the predicted decrease in repertoire diversity, polyclonal **CTL** lines and individual clones from different TdTo mice are more similar to each other than those from different wild-type mice in terms of their fingerprints of cross-reactivity to the **library** and their TCR sequences. Also, several TdTo **CTL** clones cross-react with many more **library peptides** than wild-type **CTL** clones. In a few instances, the degree of **peptide** promiscuity correlates with TCR sequence characteristics such as N region addn. and homol.-directed recombination, but not CDR3 loop length. Based on **epitope** titrns. for each clone, TCR affinity for antigen is consistently high; thus, this reduced specificity for **peptide** may coincide with an accentuated affinity for the .alpha. helixes of the **MHC**. **Peptide** promiscuity in the neonate may allow the relatively small nos. of T cells in the periphery to protect against a broader range of pathogens.

L8 ANSWER 10 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:590067 CAPLUS
DOCUMENT NUMBER: 123:53835
TITLE: Decrypting the structure of major histocompatibility complex class I-restricted cytotoxic T lymphocyte **epitopes** with complex **peptide** libraries
AUTHOR(S): Udaka, Keiko; Wiesmueller, Karl-Heniz; Kienle, Stefan; Jung, Guenther; Walden, Peter
CORPORATE SOURCE: Max-Planck-Institut Biologie, Tuebingen, D-72076, Germany
SOURCE: J. Exp. Med. (**1995**), 181(6), 2097-108
CODEN: JEMEAV; ISSN: 0022-1007
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Complex synthetic **peptide libraries** with defined amino acids in one or more positions of the H-2Kb-restricted cytotoxic T lymphocyte (**CTL**) **epitopes** SIINFEKL and RGYVYQGL and mixts. of 19 amino acids in the remaining positions were used to analyze the structural requirements of **peptide** binding to **MHC** class I mols. and antigen recognition by **CTLs**. This approach provides means to assess semiquant. the contribution of every amino acid to the binding of **peptides** to major histocompatibility complex (**MHC**) mols. without biases introduced by naturally processed **peptides**. Primary and secondary anchor residues were defined for their major contribution to the binding efficiency of the **peptides** . In contrast to primary anchors, secondary anchor amino acids vary greatly in their side chains and position in the sequences. All amino acids in the octapeptide sequences were found to exhibit pos. or neg. influences on binding to the **MHC** mols. and on recognition of the resulting complexes by **CTLs**. Strong interdependence of the effects of the individual residues in the **epitope** sequences was demonstrated. **CTL** responses to **peptide libraries** were suppressed when residues were introduced; however, they were augmented when the crit. residues of T cell recognition were fixed, suggesting a potential use of the **peptide libraries** for defining **epitope** sequences in general.

L8 ANSWER 11 OF 39 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1995:497868 CAPLUS
DOCUMENT NUMBER: 122:263117
TITLE: Isolation of a kidney-specific **peptide** recognized by alloreactive HLA-A3-restricted human CTL
AUTHOR(S): Poindexter, Nancy J.; Naziruddin, Bashoo; McCourt, David W.; Mohanakumar, T.
CORPORATE SOURCE: Dep. Surg., Howard Hughes Med. Inst., St. Louis, MO, 63110, USA
SOURCE: J. Immunol. (1995), 154(8), 3880-7
CODEN: JOIMA3; ISSN: 0022-1767
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mol. nature of tissue-specific Ags involved in **MHC** -restricted **CTL** responses is as yet undefined. To det. the specificity of these **peptides**, their function, and their possible relationship to allograft rejection, we have utilized human kidney-specific CD8+ **CTL** clones to screen reversed-phase HPLC (RP-HPLC)-sepd. self **peptides** presented by allo-class I mols. One of these clones is HLA-A3-restricted and the other HLA-B62-restricted, lysing human kidney cell lines but not **MHC** identical B lymphoblastoid cells which express the appropriate HLA mols. We have identified a biol. active RP-HPLC fraction contg. self **peptides** eluted from affinity-purified **MHC** mols. from HLA-A3+ kidney. This **peptide** is not expressed in HLA-A3+ spleen. Similarly, a HLA-B62-assocd. **peptide** fraction was identified in kidney but not in spleen using the HLA-B62-restricted **CTL** clone. Sequence anal. of the biol. active fraction from HLA-A3 kidney revealed multiple **peptides**. Because of the ambiguity of the **peptide** sequence, a mixed **peptide library** corresponding to this sequence was synthesized that included the HLA-A3 binding motif. The biol. active **peptide library** was RP-HPLC fractionated and the fraction contg. HLA-A3-restricted **CTL** activity was sequenced. The resulting sequence of the alloreactive HLA-A3-restricted **peptide epitope** is GPPGVTIVK. By using this unique strategy, we describe the successful isolation and sequencing of an antigenic **peptide** that is recognized by a human alloreactive kidney-specific **CTL** clone.

L8 ANSWER 12 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:28784 CAPLUS
DOCUMENT NUMBER: 120:28784
TITLE: **Peptide** presentation by major histocompatibility complex-class I and in vivo induction of cytotoxic T-lymphocytes
AUTHOR(S): Jung, Guenther
CORPORATE SOURCE: Inst. Org. Chem., Eberhard-Karls-Univ., Tuebingen, D-7400, Germany
SOURCE: Pept. Chem. 1992, Proc. Jpn. Symp., 2nd (1993***) , **Meeting Date 1992, 627-31. Editor(s): Yanaihara, Noboru. ESCOM: Leiden, Neth.**
CODEN: 59NTAC
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB **A review with 23 refs. on the development of novel methods for sequencing the self- ***peptide** pools isolated from **MHC**-I mols., which the authors call natural **peptide libraries**. These anal. methods are based on automated Edman degrdn. and electrospray-MS of **peptide** mixts. The sequence motifs of the self-**peptide** mixts. (natural **peptide libraries**), isolated from several **MHC**-I alleles and pool sequenced, allow the exact prediction of **CTL epitopes**. Therefore, minimal lipopeptide vaccines for in vivo elicitation of allele-specific **CTL** immune response can be constructed.

L8 ANSWER 13 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:589973 CAPLUS
DOCUMENT NUMBER: 117:189973
TITLE: Influenza basic polymerase 2 **peptides** are recognized by influenza nucleoprotein-specific cytotoxic T lymphocytes
AUTHOR(S): Anderson, Robert W.; Bennink, Jack R.; Yewdell, Jonathan W.; Maloy, W. Lee; Coligan, John E.
CORPORATE SOURCE: Biol. Resour. Branch, Natl. Inst. Allergy Infect. Dis., Bethesda, MD, 20892, USA
SOURCE: Mol. Immunol. (1992), 29(9), 1089-96
CODEN: MOIMD5; ISSN: 0161-5890
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Cytotoxic T lymphocytes (**CTL**) play an important role in limiting viral infections and in eradicating virus from host tissues. Recent progress in understanding the processing and presentation of viral antigens to **CTL** indicates that the **CTL** antigen receptor recognizes **peptides** derived from viral proteins that are bound to an antigen binding groove present in class I major histocompatibility complex (**MHC**) mols. In understanding **CTL** anti-viral responses and in creating vaccines designed to elicit **CTL** responses, it is crit. to identify the portions of viral proteins that bind class I mols. and are recognized by T cell receptors. Previous findings have indicated that a significant portion of the **CTL** response of H-2d mice to influenza virus is specific for one of the viral polymerases (PB2). To identify the region of PB2 naturally processed and presented by influenza virus-infected mouse cells to **CTL**, 31 PB2 **peptides** of 9-16 residues in length were chosen and chem. synthesized. Two **peptides**, PB2 residues 146-159 and 187-195, sensitized histocompatible target cells for recognition by influenza virus-specific **CTL**. When **CTL** were generated to individual viral proteins using influenza-vaccinia recombinant viruses, PB2-specific **CTL** failed to recognize cells sensitized with PB2 **peptides** 146-159 and 187-195. Further anal. showed that these PB2 **peptides** were, in fact, recognized by nucleoprotein (NP)-specific **CTL** generated by recombinant NP-vac virus priming and influenza A virus stimulation, or NP **peptide** stimulation in vitro of NP-vac or influenza A-primed **CTL**. Thus, while screening **peptide libraries** one cannot assume that pos. **peptides** necessarily identify the viral protein to which the **CTL** response is directed.

L8 ANSWER 14 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:629907 CAPLUS
DOCUMENT NUMBER: 115:229907
TITLE: A single amino acid substitution in an **MHC** class I molecule allows heteroclitic recognition by

lymphocytic choriomeningitis virus-specific cytotoxic T lymphocytes
AUTHOR(S): Muller, Daniel; Pederson, Katrina; Murray, Richard; Frelinger, Jeffrey A.
CORPORATE SOURCE: Dep. Microbiol. Immunol., Univ. North Carolina, Chapel Hill, NC, 27599-7290, USA
SOURCE: J. Immunol. (1991), 147(4), 1392-7
CODEN: JOIMA3; ISSN: 0022-1767
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Class I mols. of the **MHC** bind foreign and endogenous **peptides** allowing recognition by the TCR on **CTL**. The recognition and killing of cells infected with lymphocytic choriomeningitis virus (LCMV) depends on the recognition of LCMV **peptides** bound to class I **MHC**. Mutations in class I **MHC** mols. have enabled the delineation of regions in the class I mol. important for binding **peptides** and for interaction with the TCR. A **library** of class I mutants was constructed using satn. mutagenesis and a phenotypic change resulting from a single amino acid substitution is reported that results in the heteroclitic (increased) killing of LCMV-infected cells. This amino acid change, asparagine to serine at position 30, is in a conserved region of the class I mol. contacting the .alpha.3 domain. This mutation does not result in increased expression of the class I mol. on the cell surface, does not affect the binding of CD8, and does not affect allogeneic recognition. Cold target expts. show that this heterclitic killing is due to increased recognition by **CTL**. These data point toward a crit. function for this region of the class I mol. in the binding of **peptides** or their presentation to **CTL**.

L8 ANSWER 15 OF 39 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:2041 CAPLUS
DOCUMENT NUMBER: 110:2041
TITLE: The murine **MHC** class I genes, H-2Dq and H-2Lq, are strikingly homologous to each other, H-2Ld, and two genes reported to encode tumor-specific antigens
AUTHOR(S): Lee, David R.; Rubocki, Ronald J.; Lie, Wen Rong; Hansen, Ted H.
CORPORATE SOURCE: Columbia Sch. Med., Univ. Missouri, Columbia, MO, 65212, USA
SOURCE: J. Exp. Med. (1988), 168(5), 1719-39
CODEN: JEMEAV; ISSN: 0022-1007
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two phenomena appear to distinguish the D region class I genes from those in the K region in the murine **MHC**: (a) haplotype disparity in the no. of expressed D region class I mols. has been obsd.; and (b) clines of closely related D region class I mols. among and within mice of different H-2 haplotypes can be defined. Both of these observations have been based on serol. and **peptide** mapping analyses of these mols. Recent reports using mol. biol. approaches have corroborated these findings. Since the mouse strain B10.AKM expresses multiple D region class I antigens, all of which are closely related to the prototypic Ld mol., the Dq region of B10.AKM was investigated using mol. approaches. Three D region class I genes were isolated from genomic B10.AKM bacteriophage and cosmid **libraries**. Based on alignment of those genes with the BALB/c D region class I genes by analogous restriction endonuclease sites and by hybridization of one of those genes with a D4d gene-derived oligonucleotide probe, these genes were designated as Dq, Lq, and D4q. As detd. by DNA-mediated gene transfer to mouse L cells followed by serol. analyses, the Dq and Lq genes encode previously characterized Dq region class I antigens. The nuclei acid sequence comparisons of the Dq and Lq genes demonstrated a higher level of homol. with the Ld and Db genes than with other D region class I genes. In addn., **CTL** stimulated with a Dq, Lq, or Ld gene transfectant showed strong crossreactions with the other transfectants as targets, suggesting that the products of these genes are also functionally related. Thus, these studies suggest that the L mol. represents a prototypic structure shared by several D region gene products, and furthermore, that duplication of an Ld-like progenitor gene resulted in 2 Dq region class I genes, Dq and Lq. Unexpectedly, the sequences detd. for the Dq and Lq genes are nearly identical to the sequences of 2 genes, A166 and A149, resp. which were reported to encode the tumor-specific antigens; these novel class I genes were isolated from an H-2k fibrosarcoma, 1591. This raises the distinct possibility that these purported tumor-specific class I genes were introduced into this tumor by contamination.

L8 ANSWER 16 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 97054582 EMBASE
DOCUMENT NUMBER: 1997054582
TITLE: Identification of tyrosinase-related protein 2 as a tumor rejection antigen for the B16 melanoma.
AUTHOR: Bloom M.B.; Perry-Lalley D.; Robbins P.F.; Li Y.; El-Gamil M.; Rosenberg S.A.; Yang J.C.
CORPORATE SOURCE: Dr. J.C. Yang, Surgery Branch, National Cancer Institute, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, United States
SOURCE: Journal of Experimental Medicine, (1997) 185/3 (453-459).
Refs: 24
ISSN: 0022-1007 CODEN: JEMEAV
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Recently, major advances have been made in the identification of antigens from human melanoma which are recognized by T cells. In spite of this, little is known about the optimal ways to use these antigens to treat patients with cancer. Progress in this area is likely to require accurate preclinical animal models, but the availability of such models has lagged behind developments in human tumor immunology. Whereas many of the identified human melanoma antigens are normal tissue differentiation proteins, analogous murine tumor antigens have not yet been identified. In this paper we identify a normal tissue differentiation antigen, tyrosinase-related protein 2 (TRP- 2), expressed by the murine B16 melanoma which was found by screening a cDNA **library** from B16 with tumor-reactive cytotoxic T lymphocytes (**CTL**). A **peptide** conforming to the predicted **MHC** class I H2-Kb

binding motif, TRP-2181- 188, was identified as the major reactive **epitope** within TRP-2 recognized by these anti-B16 **CTLs**. By site-directed mutagenesis, it was shown that alteration of this **epitope** eliminated recognition of TRP-2. It was further demonstrated that a **CTL** line raised from splenocytes by repeated stimulation in vitro with this **peptide** could recognize B16 tumor and was therapeutic against 3-d-old established pulmonary metastases. The use of TRP-2 in a preclinical model of tumor immunotherapy may be helpful in suggesting optimal vaccination strategies for cancer therapy in patients.

L8 ANSWER 17 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 97028275 EMBASE
DOCUMENT NUMBER: 1997028275
TITLE: Cytotoxic T cell induction with ratchet **peptide** libraries.
AUTHOR: Kuebler P.J.; Nixon D.F.
CORPORATE SOURCE: D.F. Nixon, Aaron Diamond AIDS Research Center, 455, 1st Avenue, New York, NY 10016, United States
SOURCE: Vaccine, (**1996**) 14/17-18 (1664-1670).
Refs: 26
ISSN: 0264-410X CODEN: VACCDE
PUBLISHER IDENT.: S 0264-410X(96)00125-9
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
026 Immunology, Serology and Transplantation
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Immunization with synthetic **peptides** are used to induce cytotoxic T cell (**CTL**) responses in vivo. However, **CTL** **peptide** vaccines require the use of multiple **peptides** to overcome genetic diversity associated with **MHC** restriction, and prior **epitope** identification from the chosen protein template. We describe here a method whereby all nonamer sequences from a longer template can be synthesized simultaneously in a ratchet **peptide** **library** (RPL) covering all potential **epitopes** within a protein. We synthesized an RPL based on a template sequence from the Plasmodium berghei circumsporozoite (CS) protein (CSRPL). Using a lipopeptide formulation we immunized mice i.p. with the CSPRL and elicited CS specific **CTL**, which recognized the CS252-260 H-2K(d) restricted **CTL** **epitope**.

L8 ANSWER 18 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 97025254 EMBASE
DOCUMENT NUMBER: 1997025254
TITLE: Identification of potential CTL **epitopes** of bovine RSV using allele-specific **peptide** motifs from bovine **MHC** class I molecules.
AUTHOR: Gaddum R.M.; Ellis S.A.; Willis A.C.; Cook R.S.; Staines K.A.; Thomas L.H.; Taylor G.
CORPORATE SOURCE: R.M. Gaddum, Institute for Animal Health, Compton, Newbury RG20 7NN, United Kingdom
SOURCE: Veterinary Immunology and Immunopathology, (**1996**) 54/1-4 (211-219).
Refs: 50
ISSN: 0165-2427 CODEN: VIIMDS
PUBLISHER IDENT.: S 0165-2427(96)05686-3
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Conference Article
FILE SEGMENT: 004 Microbiology
015 Chest Diseases, Thoracic Surgery and Tuberculosis
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Respiratory syncytial virus (RSV) is a major cause of lower respiratory tract infection in young infants and housed calves. Depletion of CD8+ lymphocytes from calves inhibited their ability to clear the virus from the nasopharynx and lungs. To study these cells further, a cytotoxic T lymphocyte (**CTL**) assay was established. **CTL** could be demonstrated in the peripheral blood of gnotobiotic calves 7-10 days post infection (p.i.) with RSV and in lungs 10 days p.i. This response was both **MHC**-restricted and virus-specific. Following separation of the lung lymphocytes by magnetic activated cell sorting, it was shown that the cytolytic activity was mediated by cells of the CD8+ phenotype. To identify **epitopes** recognised by bovine **CTL**, the consensus motifs from **MHC** class I alleles found in the herd at Compton were identified. cDNA **libraries** were constructed and screened for full length class I sequences. The isolated cDNA clones were then transfected into mouse P815 cells and the expressed product immunoprecipitated and matched with a serological specificity. The bovine **MHC** class I molecules were isolated from lysed transfected cells by affinity chromatography, using a monoclonal antibody specific for bovine **MHC** class I, and bound **peptides** were separated by reverse-phase HPLC. Analysis of the protein sequences of bovine RSV for the defined motifs has identified potential **CTL** **epitopes**

L8 ANSWER 19 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 96225309 EMBASE
DOCUMENT NUMBER: 1996225309
TITLE: Use of combinatorial **peptide** libraries to construct functional mimics of tumor **epitopes** recognized by **MHC** class I-restricted cytolytic T lymphocytes.
AUTHOR: Blake J.; Johnston J.V.; Hellstrom K.E.; Marquardt H.; Chen L.
CORPORATE SOURCE: B.-Myers Squibb Pharma. Res. Inst., 3005 First Avenue,Seattle, WA 98121, United States
SOURCE: Journal of Experimental Medicine, (**1996**) 184/1 (121-130).
ISSN: 0022-1007 CODEN: JEMEAV
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Identification of cytolytic T lymphocyte (**CTL**) **epitopes** presented by major histocompatibility complex (**MHC**) class 1 molecules on tumor cells is critical for the design of active

immunotherapy. We describe the rise of combinatorial **peptide libraries** with defined amino acids in two **MHC** anchor positions to search for **epitopes** that are recognized by H-2Db- and Kb- restricted **CTL** specific for the mouse lymphoma EL4. An iterative strategy was used for screening **libraries** in which 16 amino acids were divided into 3 groups and 3 subgroups: .alpha.(AL, VT, FY); .beta.(GS, P, DE); .gamma.(KR, H, NQ). The proportions of each group and subgroup at individual **peptide** positions were changed in the **library** synthesis, and the effect of these changes on **CTL** activity was measured in a sensitive RMA-S cell assay. A single H-2Db **epitope** mimic was deduced from the original **library** that contained >2 x 108 potential **peptides** and was at least 9 logs more potent than the original **library**. Immunization of syngeneic mice with this **peptide** elicited **CTL** that lysed EL4 cells as well as RMA-S cells pulsed with **peptides** isolated from Db molecules of EL4 cells, indicating functional similarity between the mimicking **peptide** and the naturally processed **CTL** **epitope**. Furthermore, adoptive transfer of such a **CTL** line had a therapeutic effect in mice with EL4 established as an ascites tumor. Two H-2Kb-restricted **epitope** mimics of the same tumor were also identified. Our method represents a novel approach for the construction of **MHC** class I-restricted targets that can serve as immunogens for active immunotherapy of cancer.

L8 ANSWER 20 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 96211074 EMBASE
DOCUMENT NUMBER: 1996211074
TITLE: Self-**MHC**-restricted **peptides** recognized by an alloreactive T lymphocyte clone.
AUTHOR: Udaka K.; Wiesmuller K.-H.; Kienle S.; Jung G.; Walden P.
CORPORATE SOURCE: Dermatologische Klinik der Charite, Humboldt-Universitat, Schumannstr. 20/21,D-10117 Berlin, Germany
SOURCE: Journal of Immunology, (1996) 157/2 (670-678).
ISSN: 0022-1767 CODEN: JOIMA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Alloreactive T lymphocytes are readily detected in unprimed animals although they have never encountered the alloantigen before. This well-established phenomenon is usually explained with the assumption that a self- **MHC** molecule complexed with a defined **peptide** resembles the allo-**MHC** molecule with another **peptide** and induces the corresponding T cell specificities. Here, for the first time and in support of this hypothesis, self-**MHC**- restricted **peptides** are described for a T cell clone that was induced with allo-**MHC**. The allo-**MHC**-specific **CTL** clone 2C was derived from a H-2b mouse and recognizes H-2L(d) complexed with the naturally occurring endogenous **peptide** LSPFPFDL. H-2Kb was shown to be involved in positive selection of its TCR, and **peptides** associated with this **MHC** molecule are implicated in the process. To identify such **peptides**, positional scanning with random **peptide libraries** combined with an iterative approach was employed. Several active **peptides** were found and the most efficient, SIYRYYGL, was chosen for further studies. Recognition by 2C of the two **MHC-peptide** adducts H-2L(d) + LSPFPFDL and H-2K(b) + SIYRYYGL is mediated by the same TCR and appears to be similarly efficient as concluded from inhibition experiments with an Id- specific Ab. **CTLs** from SIYRYYGL-primed H-2b mice respond to H-2L(d) + LSPFPFDL. This reciprocal cross-reactivity suggests that structural features are shared by the two **MHC-peptide** complexes.

L8 ANSWER 21 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 96144399 EMBASE
DOCUMENT NUMBER: 1996144399
TITLE: Specificity and degeneracy of minor histocompatibility antigen-specific **MHC**-restricted CTL.
AUTHOR: Gundlach B.R.; Wiesmuller K.-H.; Junt T.; Kienle S.; Jung G.; Walden P.
CORPORATE SOURCE: Dermatologische Klinik, Humboldt-Universitat, Schumannstr. 20/21,D-10117 Berlin, Germany
SOURCE: Journal of Immunology, (1996) 156/10 (3645-3651).
ISSN: 0022-1767 CODEN: JOIMA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Random **peptide libraries** were employed to investigate the specificity of Ag recognition by H-3-specific, H-2Kb-restricted **CTL** clones. The **peptide libraries** consist of octapeptides with one defined sequence position and mixtures of 19 amino acids (all proteinogenic amino acids except for cysteine) in the remaining seven sequence positions. The complete set of 152 **peptide libraries** includes all octapeptides possible with these amino acids. Responses of the **CTL** clones to these **peptide libraries** reveal patterns of preferred **epitope** amino acids. Depending on the **CTL** clone tested, varying numbers of different amino acids were identified for the different sequence positions indicating degeneracy of Ag recognition. Sequences for synthetic **epitopes** active at low pM concentrations could be deduced from these patterns: They confirm that TCRs of **CTL** clones do not exhibit specificity for unique ligand structures but rather can interact with sets of ligands. The sequences of **peptides** recognized by a single clone exhibit great sequence heterogeneity.

L8 ANSWER 22 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 96083797 EMBASE
DOCUMENT NUMBER: 1996083797
TITLE: Increased **peptide** promiscuity provides a rationale for the lack of N regions in the neonatal T cell repertoire.
AUTHOR: Gavin M.A.; Bevan M.J.
CORPORATE SOURCE: Department of Immunology, Howard Hughes Medical Institute, University of Washington,Seattle, WA 98195-7370, United States
SOURCE: Immunity, (1995) 3/6 (793-800).
ISSN: 1074-7613 CODEN: IUNIEH
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics

025 Hematology
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Making use of mice deficient for terminal deoxynucleotidyl transferase (TdT) expression and a random **peptide library**, we have examined the diversity and **peptide** specificity of the neonatal T cell repertoire specific for a single H-2D(b)-restricted **peptide** . Consistent with the predicted decrease in repertoire diversity, polyclonal **CTL** lines and individual clones from different TdT(o) mice are more similar to each other than those from different wild-type mice in terms of their fingerprints of cross-reactivity to the **library** and their TCR sequences. We have also found that several TdT(o) **CTL** clones cross-react with many more **library** **peptides** than wild-type **CTL** clones. In a few instances, the degree of **peptide** promiscuity correlates with TCR sequence characteristics such as N region addition and homology-directed recombination, but not CDR3 loop length. Based on **epitope** titrations for each clone, TCR affinity for antigen is consistently high; thus, this reduced specificity for **peptide** may coincide with an accentuated affinity for the a helices of the **MHC**. **Peptide** promiscuity in the neonate may allow the relatively small numbers of T cells in the periphery to protect against a broader range of pathogens.

L8 ANSWER 23 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 95169729 EMBASE
DOCUMENT NUMBER: 1995169729
TITLE: Decrypting the structure of major histocompatibility complex class I- restricted cytotoxic T lymphocyte **epitopes** with complex **peptide** libraries.
AUTHOR: Udaka K.; Wiesmuller K.-H.; Kienle S.; Jung G.; Walden P.
CORPORATE SOURCE: Max-Planck-Institut fur Biologie, Abteilung Immungenetik, Corrensstrasse 42,D-72076 Tubingen, Germany
SOURCE: Journal of Experimental Medicine, (1995) 181/6 (2097-2108).
ISSN: 0022-1007 CODEN: JEMEAV
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 006 Internal Medicine
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Complex synthetic **peptide libraries** with defined amino acids in one or more positions of the H-2Kb-restricted cytotoxic T lymphocyte (**CTL**) **epitopes** SIINFEKL and RGYVYQGL and mixtures of 19 amino acids in the remaining positions were used to analyze the structural requirements of **peptide** binding to **MHC** class I molecules and antigen recognition by **CTLs**. This approach provides means to assess semiquantitatively the contribution of every amino acid to the binding of **peptides** to major histocompatibility complex (**MHC**) molecules without biases introduced by naturally processed **peptides**. Primary and secondary anchor residues were defined for their major contribution to the binding efficiency of the **peptides**. In contrast to primary anchors, secondary anchor amino acids vary greatly in their side chains and position in the sequences. All amino acids in the octapeptide sequences were found to exhibit positive or negative influences on binding to the **MHC** molecules and on recognition of the resulting complexes by **CTLs**. Strong interdependence of the effects of the individual residues in the **epitope** sequences was demonstrated. **CTL** responses to **peptide libraries** were suppressed when residues were introduced; however, they were augmented when the critical residues for T cell recognition were fixed, suggesting a potential use of the **peptide libraries** for defining **epitope** sequences in general.

L8 ANSWER 24 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 95116981 EMBASE
DOCUMENT NUMBER: 1995116981
TITLE: Isolation of a kidney-specific **peptide** recognized by alloreactive HLA-A3- restricted human CTL.
AUTHOR: Poindexter N.J.; Naziruddin B.; McCourt D.W.; Mohanakumar T.
CORPORATE SOURCE: Department of Surgery, Washington Univ. School of Medicine, 4939 Children's Place,St. Louis, MO 63110, United States
SOURCE: Journal of Immunology, (1995) 154/8 (3880-3887).
ISSN: 0022-1767 CODEN: JOIMA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The molecular nature of tissue-specific Ags involved in **MHC** -restricted **CTL** responses is as yet undefined. To determine the specificity of these **peptides**, their function, and their possible relationship to allograft rejection, we have utilized human kidney-specific CD8+ **CTL** clones to screen reversed-phase HPLC (RP-HPLC)-separated self **peptides** presented by allo- class I molecules. One of these clones is HLA-A3-restricted and the other HLA-B62-restricted, lysing human kidney cell lines but not **MHC** identical B lymphoblastoid cells which express the appropriate HLA molecules. We have identified a biologically active RP-HPLC fraction containing self **peptides** eluted from affinity-purified **MHC** molecules from HLA-A3+ kidney. This **peptide** is not expressed in HLA-A3+ spleen. Similarly, a HLA-B62-associated **peptide** fraction was identified in kidney but not in spleen using the HLA- B62-restricted **CTL** clone. Sequence analysis of the biologically active fraction from HLA-A3 kidney revealed multiple **peptides**. Because of the ambiguity of the **peptide** sequence, a mixed **peptide library** corresponding to this sequence was synthesized that included the HLA-A3 binding motif. The biologically active **peptide library** was RP-HPLC fractionated and the fraction containing HLA-A3-restricted **CTL** activity was sequenced. The resulting sequence of the alloreactive HLA-A3-restricted **peptide epitope** is GPPGVTIVK. By using this unique strategy, we describe the successful isolation and sequencing of an antigenic **peptide** that is recognized by a human alloreactive kidney-specific **CTL** clone.

L8 ANSWER 25 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 92251943 EMBASE

DOCUMENT NUMBER: 1992251943
TITLE: Influenza basic polymerase 2 **peptides** are recognized by influenza nucleoprotein-specific cytotoxic T lymphocytes.
AUTHOR: Anderson R.W.; Bennink J.R.; Yewdell J.W.; Maloy W.L.; Coligan J.E.
CORPORATE SOURCE: Biological Resources Branch, NIAID, NIH,Bethesda, MD 20892, United States
SOURCE: Molecular Immunology, (**1992**) 29/9 (1089-1096).
ISSN: 0161-5890 CODEN: IMCHAZ
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Cytotoxic T lymphocytes (**CTL**) play an important role in limiting viral infections and in eradicating virus from host tissues. Recent progress in understanding the processing and presentation of viral antigens to **CTL** indicates that the **CTL** antigen receptor recognizes **peptides** derived from viral proteins that are bound to an antigen binding groove present in class I major histocompatibility complex (**MHC**) molecules. In understanding **CTL** anti-viral responses and in creating vaccines designed to elicit **CTL** responses, it is critical to identify the portions of viral proteins that bind class I molecules and are recognized by T cell receptors. Previous findings have indicated that a significant portion of the **CTL** response of H-2(d) mice to influenza virus is specific for one of the viral polymerases (PB2). To identify the region of PB2 naturally processed and presented by influenza virus-infected mouse cells to **CTL**, 31 PB2 **peptides** of 9-16 residues in length were chosen and chemically synthesized. Two **peptides**, PB2, residues 146-159 and 187-195, were found to sensitize histocompatible target cells for recognition by influenza virus-specific **CTL**. When **CTL** were generated to individual viral proteins using influenza-vaccinia recombinant viruses, we found, to our surprise, that PB2-specific **CTL** failed to recognize cells sensitized with PB2 **peptides** 146-159 and 187-195. Further analysis showed that these PB2 **peptides** were, in fact, recognized by nucleoprotein (NP)-specific **CTL** generated by NP-vac virus priming and influenza A virus stimulation, or NP **peptide** stimulation in vitro of NP-vac or influenza A-primed **CTL**. These results demonstrate that while screening **peptide libraries** one cannot assume that positive **peptides** necessarily identify the viral protein to which the **CTL** response is directed.

L8 ANSWER 26 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 91275192 EMBASE
DOCUMENT NUMBER: 1991275192
TITLE: A single amino acid substitution in an **MHC** class I molecule allows heteroclitic recognition by lymphocytic choriomeningitis virus-specific cytotoxic T lymphocytes.
AUTHOR: Muller D.; Pederson K.; Murray R.; Frelinger J.A.
CORPORATE SOURCE: Microbiology/Immunology Dept., University of North Carolina,Chapel Hill, NC 27599-7290, United States
SOURCE: Journal of Immunology, (**1991**) 147/4 (1392-1397).
ISSN: 0022-1767 CODEN: JOIMA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Conference Article
FILE SEGMENT: 026 Immunology, Serology and Transplantation
047 Virology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Class I molecules of the **MHC** bind foreign and endogenous **peptides** allowing recognition by the TCR on **CTL**. The recognition and killing of cells infected with lymphocytic choriomeningitis virus (LCMV) depends on the recognition of LCMV **peptides** bound to class I **MHC**. Mutations in class I **MHC** molecules have enabled the delineation of regions in the class I molecule important for binding **peptides** and for interaction with the TCR. We have constructed a **library** of class I mutants using saturation mutagenesis and report a phenotypic change resulting from a single amino acid substitution that results in the heteroclitic (increased) killing of LCMV-infected cells. This amino acid change, asparagine to serine at position 30, is in a conserved region of the class I molecule contacting the .alpha.3 domain. This mutation does not result in increased expression of the class I molecule on the cell surface, does not affect the binding of CD8, and does not affect allogeneic recognition. Cold target experiments show that this heteroclitic killing is due to increased recognition by **CTL**. These data point toward a critical function for this region of the class I molecule in the binding of **peptides** or their presentation to **CTL**.

L8 ANSWER 27 OF 39 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 89023259 EMBASE
DOCUMENT NUMBER: 1989023259
TITLE: The murine **MHC** class I genes, H-2D(q) and H-2L(q), are strikingly homologous to each other, H-2L(d), and two genes reported to encode tumor-specific antigens.
AUTHOR: Lee D.R.; Rubocki R.J.; Lie W.-R.; Hansen T.H.
CORPORATE SOURCE: Department of Microbiology, University of Missouri-Columbia School of Medicine, Columbia, MO 65212, United States
SOURCE: Journal of Experimental Medicine, (**1988**) 168/5 (1719-1739).
ISSN: 0022-1007 CODEN: JEMEAV
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 022 Human Genetics
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Two phenomena appear to distinguish the D region class I genes from those in the K region in the murine **MHC**: (a) haplotype disparity in the number of expressed D region class I molecules has been observed; and (b) clines of closely related D region class I molecules among and within mice of different H-2 haplotypes can be defined. Both of these observations have been based on serological and **peptide** mapping analyses of these molecules. Recent reports using molecular biological approaches have corroborated these findings. Since the mouse strain B10.AKM expresses multiple D region class I antigens, all of which are closely related to the prototypic L(d) molecule, we investigated the D(q) region of B10.AKM using molecular approaches. Three D region class I genes were isolated from genomic B10.AKM bacteriophage and cosmid

libraries. Based on alignment of those genes with the BALB/c D region class I genes by analogous restriction endonuclease sites and by hybridization of one of those genes with a D4(d) gene-derived oligonucleotide probe, we have designated these genes as D(q), L(q), and D4(q). As determined by DNA mediated gene transfer to mouse L cells followed by serological analyses, the D(q) and L(q) genes encode previously characterized D(q) region class I antigens. The nucleic acid sequence comparisons of the D(q) and L(q) genes demonstrated a higher level of homology with the L(d) and Db genes than with other D region class I genes. In addition, **CTL** stimulated with a D(q), L(q), or L(d) gene transfectant showed strong crossreactions with the other transfectants as targets, suggesting that the products of these genes are also functionally related. Thus, these studies suggest that the L molecule represents a prototypic structure shared by several D region gene products, and furthermore, that duplication of an L(d)-like progenitor gene resulted in two D(q) region class I genes, D(q) and L(q). Unexpectedly, the sequences determined for the D(q) and L(q) genes are nearly identical to the sequences of two genes, A166 and A149, respectively, which were reported to encode the tumor-specific antigens; these novel class I genes were isolated from an H-2(k) fibrosarcoma, 1591. This raises the distinct possibility that these purported tumor-specific class I genes were introduced into this tumor by contamination.

L8 ANSWER 28 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:386470 BIOSIS
DOCUMENT NUMBER: PREV199799685673
TITLE: Antigen processing by proteasomes: Insights into the molecular basis of crypticity.
AUTHOR(S): Djaballah, Hakim
CORPORATE SOURCE: MRC Transplantation Biol. Group, Royal Postgrad. Med. Sch., Hammersmith Hosp., Du Cane Road, London W12 0NN UK
SOURCE: Molecular Biology Reports, (1997) Vol. 24, No. 1-2, pp. 63-67.
ISSN: 0301-4851.
DOCUMENT TYPE: General Review
LANGUAGE: English
AB Eight to eleven amino acid residues are the sizes of predominant **peptides** found to be associated with **MHC** class I molecules. Proteasomes have been implicated in antigen processing and generation of such **peptides**. Advanced methodologies in **peptide** elution together with sequence determination have led to the characterization of **MHC** class I binding motifs. More recently, screening of random **peptide** phage display **libraries** and synthetic combinatorial **peptide** **libraries** have also been successfully used. This has led to the development and use of predictive algorithms to screen antigens for potential **CTL epitopes**. Not all predicted **epitopes** will be generated in vivo and the emerging picture suggests differential presentation of predicted **CTL** **epitopes** ranging from cryptic to immunodominant. The scope of this review is to discuss antigen processing by proteasomes, and to put forward a hypothesis that the molecular basis of immunogenicity can be a function of proteasomal processing. This may explain how pathogens and tumours are able to escape immunosurveillance by altering sequences required by proteasomes for **epitope** generation.

L8 ANSWER 29 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:119732 BIOSIS
DOCUMENT NUMBER: PREV199799426235
TITLE: Identification of tyrosinase-related protein 2 as a tumor rejection antigen for the B16 melanoma.
AUTHOR(S): Bloom, Matthew B.; Perry-Lalley, Donna; Robbins, Paul F.; Li, Yong; El-Gamil, Mona; Rosenberg, Steven A.; Yang, James C.
CORPORATE SOURCE: Surg. Branch, National Cancer Inst., National Inst. Health, Bethesda, MD 20892 USA
SOURCE: Journal of Experimental Medicine, (1997) Vol. 185, No. 3, pp. 453-459.
ISSN: 0022-1007.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Recently, major advances have been made in the identification of antigens from human melanoma which are recognized by T cells. In spite of this, little is known about the optimal ways to use these antigens to treat patients with cancer. Progress in this area is likely to require accurate preclinical animal models, but the availability of such models has lagged behind developments in human tumor immunology. Whereas many of the identified human melanoma antigens are normal tissue differentiation proteins, analogous murine tumor antigens have not yet been identified. In this paper we identify a normal tissue differentiation antigen, tyrosinase-related protein 2 (TRP-2), expressed by the murine B16 melanoma which was found by screening a cDNA **library** from B16 with tumor-reactive cytotoxic T lymphocytes (**CTL**). A **peptide** conforming to the predicted **MHC** class I H2-K-b binding motif, TRP-2-181-188, was identified as the major reactive **epitope** within TRP-2 recognized by these anti-B16 **CTLs**. By site-directed mutagenesis, it was shown that alteration of this **epitope** eliminated recognition of TRP-2. It was further demonstrated that a **CTL** line raised from splenocytes by repeated stimulation in vitro with this **peptide** could recognize B16 tumor and was therapeutic against 3-d-old established pulmonary metastases. The use of TRP-2 in a preclinical model of tumor immunotherapy may be helpful in suggesting optimal vaccination strategies for cancer therapy in patients.

L8 ANSWER 30 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1997:111284 BIOSIS
DOCUMENT NUMBER: PREV199799410487
TITLE: Cytotoxic T cell induction with ratchet **peptide** libraries.
AUTHOR(S): Kuebler, Peter J.; Nixon, Douglas F. (1)
CORPORATE SOURCE: (1) Aaron Diamond AIDS Res. Cent., 455, 1st Avenue, New York, NY 10016 USA
SOURCE: Vaccine, (1996) Vol. 14, No. 17-18, pp. 1664-1670.
ISSN: 0264-410X.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Immunization with synthetic **peptides** are used to induce cytotoxic T cell (**CTL**) responses in vivo. However, **CTL** **peptide** vaccines require the use of multiple **peptides** to overcome genetic diversity associated with **MHC** restriction, and prior **epitope** identification from the chosen protein template. We describe here a method whereby all nonamer sequences from a longer

template can be synthesized simultaneously in a ratchet **peptide library** (RPL) covering all potential **epitopes** within a protein. We synthesized an RPL based on a template sequence from the Plasmodium berghei circumsporozoite (CS) protein (CSRPL). Using a lipopeptide formulation we immunized mice i. p. with the CSRPL and elicited CS specific **CTL**, which recognized the CS252-260 H-2K-d restricted **CTL epitope**.

L8 ANSWER 31 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1996:383101 BIOSIS
DOCUMENT NUMBER: PREV199699105457
TITLE: Use of combinatorial **peptide** libraries to construct functional mimics of tumor **epitopes** recognized by **MHC** class I-restricted cytolytic T lymphocytes.
AUTHOR(S): Blake, James; Johnston, Janet V.; Hellstrom, Karl Erik; Marquardt, Hans; Chen, Lieping (1)
CORPORATE SOURCE: (1) Bristol-Myers Squibb Pharmaceutical Res. Inst., 3005 First Ave., Seattle, WA 98121 USA
SOURCE: Journal of Experimental Medicine, (1996) Vol. 184, No. 1, pp. 121-130.
ISSN: 0022-1007.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Identification of cytolytic T lymphocyte (**CTL**) **epitopes** presented by major histocompatibility complex (**MHC**) class I molecules on tumor cells is critical for the design of active immunotherapy. We describe the use of combinatorial **peptide libraries** with defined amino acids in two **MHC** anchor positions to search for **epitopes** that are recognized by H-2D-b- and K-b- restricted **CTL** specific for the mouse lymphoma EL4. An iterative strategy was used for screening **libraries** in which 16 amino acids were divided into 3 groups and 3 subgroups: alpha(AL, VT, FY); beta(GS, P, DE); gamma(KR, H, NQ). The proportions of each group and subgroup at individual **peptide** positions were changed in the **library** synthesis, and the effect of these changes on **CTL** activity was measured in a sensitive RMA-S cell assay. A single H-2D-b **epitope** mimic was deduced from the original **library** that contained gt 2 times 10-8 potential **peptides** and was at least 9 logs more potent than the original **library**. Immunization of syngeneic mice with this **peptide** elicited **CTL** that lysed EL4 cells as well as RMA-S cells pulsed with **peptides** isolated from D-b molecules of EL4 cells, indicating functional similarity between the mimicking **peptide** and the naturally processed **CTL epitope**. Furthermore, adoptive transfer of such a **CTL** line had a therapeutic effect in mice with EL4 established as an ascites tumor. Two H-2K-b-restricted **epitope** mimics of the same tumor were also identified. Our method represents a novel approach for the construction of **MHC** class I-restricted targets that can serve as immunogens for active immunotherapy of cancer.

L8 ANSWER 32 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1996:381263 BIOSIS
DOCUMENT NUMBER: PREV199699103619
TITLE: Self-**MHC**-restricted **peptides** recognized by an alloreactive T lymphocyte clone.
AUTHOR(S): Udaka, Keiko; Wiesmueller, Karl-Heinz; Kienle, Stefan; Jung, Guenther; Walden, Peter (1)
CORPORATE SOURCE: (1) Dermatologische Klinik der Charite, Humbolt-Univ., Schumannstr. 20/21, D-10117 Berlin Germany
SOURCE: Journal of Immunology, (1996) Vol. 157, No. 2, pp. 670-678.
ISSN: 0022-1767.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Alloreactive T lymphocytes are readily detected in unprimed animals although they have never encountered the alloantigen before. This well-established phenomenon is usually explained with the assumption that a self-**MHC** molecule complexed with a defined **peptide** resembles the allo-**MHC** molecule with another **peptide** and induces the corresponding T cell specificities. Here, for the first time and in support of this hypothesis, self-**MHC**-restricted **peptides** are described for a T cell clone that was induced with allo-**MHC**. The allo-**MHC**-specific **CTL** clone 2C was derived from a H-2-b mouse and recognizes H-2L-d complexed with the naturally occurring endogenous **peptide** LSPFPFDL. H-2K-b was shown to be involved in positive selection of its TCR, and **peptides** associated with this **MHC** molecule are implicated in the process. To identify such **peptides**, positional scanning with random **peptide libraries** combined with an iterative approach was employed. Several active **peptides** were found and the most efficient, SIYRYYGL, was chosen for further studies. Recognition by 2C of the two **MHC-peptide** adducts H-2L-d+ LSPFPFDL and H-2K-b + SIYRYYGL is mediated by the same TCR and appears to be similarly efficient as concluded from inhibition experiments with an Id-specific Ab. **CTLs** from SIYRYYGL-primed H-2-b mice respond to H-2L-d + LSPFPFDL. This reciprocal cross-reactivity suggests that structural features are shared by the two **MHC-peptide** complexes.

L8 ANSWER 33 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1996:284018 BIOSIS
DOCUMENT NUMBER: PREV199699006374
TITLE: Specificity and degeneracy of minor histocompatibility antigen-specific **MHC**-restricted CTL.
AUTHOR(S): Gundlach, Bjorn R.; Wiesmueller, Karl-Heinz; Junt, Tobias; Kienle, Stefan; Jung, Guenther; Walden, Peter (1)
CORPORATE SOURCE: (1) Dermatol. Klinik, Charite, Humboldt-Universitaet, Schumannstr. 20/21, D-10117 Berlin Germany
SOURCE: Journal of Immunology, (1996) Vol. 156, No. 10, pp. 3645-3651.
ISSN: 0022-1767.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Random **peptide libraries** were employed to investigate the specificity of Ag recognition by H-3-specific, H-2K-b-restricted **CTL** clones. The **peptide libraries** consist of octapeptides with one defined sequence position and mixtures of 19 amino acids (all proteinogenic amino acids except for cysteine) in the remaining seven sequence positions. The complete set of 152 **peptide libraries** includes all octapeptides possible with these amino acids. Responses of the **CTL** clones to these **peptide libraries** reveal patterns of preferred **epitope** amino

acids. Depending on the **CTL** clone tested, varying numbers of different amino acids were identified for the different sequence positions indicating degeneracy of Ag recognition. Sequences for synthetic **epitopes** active at low pM concentrations could be deduced from these patterns. They confirm that TCRs of **CTL** clones do not exhibit specificity for unique ligand structures but rather can interact with sets of ligands. The sequences of **peptides** recognized by a single clone exhibit great sequence heterogeneity.

L8 ANSWER 34 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1995:309438 BIOSIS
DOCUMENT NUMBER: PREV199598323738
TITLE: Decrypting the Structure of Major Histocompatibility Complex Class I-Restricted Cytotoxic T Lymphocytes **Epitopes** with Complex **Peptide** Libraries.
AUTHOR(S): Udaka, Keiko; Wiesmueller, Karl-Heinz; Kienle, Stefan; Jung, Guenther; Walden, Peter (1)
CORPORATE SOURCE: (1) Max Planck Inst. Biol., Abteilung Immungenet., Corrensstrasse 42, D-72076 Tuebingen Germany
SOURCE: Journal of Experimental Medicine, (1995) Vol. 181, No. 6, pp. 2097-2108.
ISSN: 0022-1007.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Complex synthetic **peptide libraries** with defined amino acids in one or more positions of the H-2K-b-restricted cytotoxic T lymphocyte (**CTL**) **epitopes** SIINFEKL and RGYVYQGL and mixtures of 19 amino acids in the remaining positions were used to analyze the structural requirements of **peptide** binding to **MHC** class I molecules and antigen recognition by **CTLs**. This approach provides means to assess semiquantitatively the contribution of every amino acid to the binding of **peptides** to major histocompatibility complex (**MHC**) molecules without biases introduced by naturally processed **peptides**. Primary and secondary anchor residues were defined for their major contribution to the binding efficiency of the **peptides**. In contrast to primary anchors, secondary anchor amino acids vary greatly in their side chains and position in the sequences. All amino acids in the octapeptide sequences were found to exhibit positive or negative influences on binding to the **MHC** molecules and on recognition of the resulting complexes by **CTLs**. Strong interdependence of the effects of the individual residues in the **epitope** sequences was demonstrated. **CTL** responses to **peptide libraries** were suppressed when residues were introduced; however, they were augmented when the critical residues for T cell recognition were fixed, suggesting a potential use of the **peptide libraries** for defining **epitope** sequences in general.

L8 ANSWER 35 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1995:221511 BIOSIS
DOCUMENT NUMBER: PREV199598235811
TITLE: Isolation of a kidney-specific **peptide** recognized by alloreactive HLA-A3-restricted human CTL.
AUTHOR(S): Poindexter, Nancy J.; Naziruddin, Bashoo; McCourt, David W.; Mohanakumar, T. (1)
CORPORATE SOURCE: (1) Dep. Surgery, P.O. Box 8109-CSRB 4449, Washington Univ. Sch. Med., 4939 Children's Place, St. Louis, MO 63110 USA
SOURCE: Journal of Immunology, (1995) Vol. 154, No. 8, pp. 3880-3887.
ISSN: 0022-1767.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The molecular nature of tissue-specific Ags involved in **MHC** -restricted **CTL** responses is as yet undefined. To determine the specificity of these **peptides**, their function, and their possible relationship to allograft rejection, we have utilized human kidney-specific CD8+ **CTL** clones to screen reversed-phase HPLC (RP-HPLC)-separated self **peptides** presented by allo-class I molecules. One of these clones is HLA-A3-restricted and the other HLA-B62-restricted, lysing human kidney cell lines but not **MHC** identical B lymphoblastoid cells which express the appropriate HLA molecules. We have identified a biologically active RP-HPLC fraction containing self **peptides** eluted from affinity-purified **MHC** molecules from HLA-A3+ kidney. This **peptide** is not expressed in HLA-A3+ spleen. Similarly, a HLA-B62-associated **peptide** fraction was identified in kidney but not in spleen using the HLA-B62-restricted **CTL** clone. Sequence analysis of the biologically active fraction from HLA-A3 kidney revealed multiple **peptides**. Because of the ambiguity of the **peptide** sequence, a mixed **peptide library** corresponding to this sequence was synthesized that included the HLA-A3 binding motif. The biologically active **peptide library** was RP-HPLC fractionated and the fraction containing HLA-A3-restricted **CTL** activity was sequenced. The resulting sequence of the alloreactive HLA-A3-restricted **peptide epitope** is GPPGVTIVK. By using this unique strategy, we describe the successful isolation and sequencing of an antigenic **peptide** that is recognized by a human alloreactive kidney-specific **CTL** clone.

L8 ANSWER 36 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1994:406226 BIOSIS
DOCUMENT NUMBER: PREV199497419226
TITLE: Class I **MHC-peptide** interaction: Structural and functional aspects.
AUTHOR(S): Ruppert, J.; Kubo, R. T.; Sidney, J.; Grey, H. M.; Sette, A.
CORPORATE SOURCE: Cytel, 3525 John Hopkins Court, San Diego, CA 92121 USA
SOURCE: Behring Institute Mitteilungen, (1994) Vol. 0, No. 94, pp. 48-60.
ISSN: 0301-0457.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The structural requirements for the interaction between antigens and class I molecules was investigated through the use of a quantitative assay to measure **peptide** binding to different **MHC** class I alleles. We determined the permissiveness of the main anchors reported by Rammensee and his group for **peptide** binding and defined an extended motif for **peptides** binding to the HLA-A2.1 allele, including the role of non-anchor positions. It was found that the main anchors were necessary, but not sufficient, for good binding. Certain non-anchor positions contributed significantly to overall binding and were referred to as secondary anchors. This finding allowed a better prediction

of high affinity binding **peptides** selected from **libraries** of different viral and tumor proteins. Furthermore, our data allowed correlation of the structural requirements for binding of **peptides** with crystallographic data of the **MHC** molecule. In order to characterize allele-specific motifs for a larger number of alleles, the HLA-A alleles A1, A3, A11, and A24, which represent some of the most common alleles found in different ethnic populations, were chosen. Here, most motifs were found to be highly exclusive; however, HLA-A3 and A11 shared a common motif. The defined motifs were validated further by using naturally processed **peptides**. Those **peptides** were also synthesized and tested for binding to the appropriate HLA alleles, giving a binding affinity from 0.3 to 200 nM for sequences of naturally processed **peptides**. Finally, a set of all possible 9-mer **peptides** from HPV 16 proteins were synthesized and tested for binding to the five class I alleles. For each allele, high affinity binders were identified, thus allowing for selection of possible **peptide** candidates for a **CTL** based vaccine.

L8 ANSWER 37 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1992:477182 BIOSIS
DOCUMENT NUMBER: BA94:108557
TITLE: INFLUENZA BASIC POLYMERASE 2 **PEPTIDES** ARE RECOGNIZED BY INFLUENZA NUCLEOPROTEIN-SPECIFIC CYTOTOXIC T LYMPHOCYTES.
AUTHOR(S): ANDERSON R W; BENNINK J R; YEWDELL J W; MALOY W L; COLIGAN J E
CORPORATE SOURCE: BIOLOGICAL RESOURCES BRANCH, NIAID, NIH, BUILD., 4, ROOM 413, BETHESDA, MD. 20892.
SOURCE: MOL IMMUNOL, (1992) 29 (9), 1089-1096.
CODEN: MOIMD5. ISSN: 0161-5890.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Cytotoxic T lymphocytes (**CTL**) play an important role in limiting viral infections and in eradicating virus from host tissues. Recent progress in understanding the processing and presentation of viral antigens to **CTL** indicates that the **CTL** antigen receptor recognizes **peptides** derived from viral proteins that are bound to an antigen binding groove present in class I major histocompatibility complex (**MHC**) molecules. In understanding **CTL** anti-viral responses and in creating vaccines designed to elicit **CTL** responses, it is critical to identify the portions of viral proteins that bind class I molecules and are recognized by T cell receptors. Previous findings have indicated that a significant portion of the **CTL** response of H-2d mice to influenza virus is specific for one of the viral polymerases (PB2). To identify the region of PB2 naturally processed and presented by influenza virus-infected mouse cells to **CTL**, 31 PB2 **peptides** of 9-16 residues in length were chosen and chemically synthesized. Two **peptides**, PB2, residues 146-159 and 187-195, were found to sensitize histocompatible target cells for recognition by influenza virus-specific **CTL**. When **CTL** were generated to individual viral proteins using influenza-vaccinia recombinant viruses, we found, to our surprise, that PB2-specific **CTL** failed to recognize cells sensitized with PB2 **peptides** 146-159 and 187-195. Further analysis showed that these PB2 **peptides** were, in fact, recognized by nucleoprotein (NP)-specific **CTL** generated by NP-vac virus priming and influenza A virus stimulation, or NP **peptide** stimulation in vitro of NP-vac or influenza A-primed **CTL**. These results demonstrate that while screening **peptide libraries** one cannot assume that positive **peptides** necessarily identify the viral protein to which the **CTL** response is directed.

L8 ANSWER 38 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1991:455244 BIOSIS
DOCUMENT NUMBER: BA92:100024
TITLE: A SINGLE AMINO ACID SUBSTITUTION IN AN **MHC** CLASS I MOLECULE ALLOWS HETEROCLITIC RECOGNITION BY LYMPHOCYTIC CHORIOMENINGITIS VIRUS-SPECIFIC CYTOTOXIC T LYMPHOCYTES.
AUTHOR(S): MULLER D; PEDERSON K; MURRAY R; FRELINGER J A
CORPORATE SOURCE: DEP. MICROBIOL. IMMUNOL., UNIV. NORTH CAROLINA, CHAPEL HILL, N.C. 27599-7290.
SOURCE: J IMMUNOL, (1991) 147 (4), 1392-1397.
CODEN: JOIMA3. ISSN: 0022-1767.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Class I molecules of the **MHC** bind foreign and endogenous **peptides** allowing recognition by the TCR on **CTL**. The recognition and killing of cells infected with lymphocytic choriomeningitis virus (LCMV) depends on the recognition of LCMV **peptides** bound to class I **MHC**. Mutations in class I **MHC** molecules have enabled the delineation of regions in the class I molecule important for binding **peptides** and for interaction with the TCR. We have constructed a **library** of class I mutants using saturation mutagenesis and report a phenotypic change resulting from a single amino acid substitution that results in the heteroclitic (increased) killing of LCMV-infected cells. This amino acid change, asparagine to serine at position 30, is in a conserved region of the class I molecule contacting the .alpha.3 domain. This mutation does not result in increased expression of the class I molecule on the cell surface, does not affect the binding of CD8, and does not affect allogeneic recognition. Cold target experiments show that this heteroclitic killing is due to increased recognition by **CTL**. These data point toward a critical function for this region of the class I molecule in the binding of **peptides** or their presentation to **CTL**.

L8 ANSWER 39 OF 39 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:75020 BIOSIS
DOCUMENT NUMBER: BA87:39418
TITLE: THE MURINE **MHC** CLASS I GENES H-2D-Q AND H-2L-Q ARE STRIKINGLY HOMOLOGOUS TO EACH OTHER H-2L-D AND TWO GENES REPORTED TO ENCODE TUMOR-SPECIFIC ANTIGENS.
AUTHOR(S): LEE D R; RUBOCKI R J; LIE W-R; HANSEN T H
CORPORATE SOURCE: DEP. MICROBIOL., UNIV. MO.-COLUMBIA SCH. MED., COLUMBIA, MO. 65212.
SOURCE: J EXP MED, (1988) 168 (5), 1719-1740.
CODEN: JEMEAV. ISSN: 0022-1007.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Two phenomena appear to distinguish the D region class I genes from those in the K region in the murine **MHC**: (a) haplotype disparity in the number of expressed D region class I molecules has been observed; and (b) clines of closely related D region class I molecules among and within

mice of different H-2 haplotypes can be defined. Both of these observations have been based on serological and **peptide** mapping analyses of these molecules. Recent reports using molecular biological approaches have corroborated these findings. Since the mouse strain B10.AKM expresses multiple D region class I antigens, all of which are closely related to the prototypic Ld molecule, we investigated the Dq region of B10.AKM using molecular approaches. Three D region class I genes were isolated from genomic B10.AKM bacteriophage and cosmid **libraries**. Based on alignment of those genes with the BALB/c D region class I genes by analogous restriction endonuclease sites and by hybridization of one of those genes with a D4d gene-derived oligonucleotide probe, we have designated these genes as Dq, Lq, and D4q. As determined by DNA-mediated gene transfer to mouse L cells followed by serological analyses, the Dq and Lq genes encode previously characterized Dq region class I antigens. The nucleic acid sequence comparisons of the Dq and Lq genes demonstrated a higher level of homology with the Ld and Db genes than with other D region class I genes. In addition, **CTL** stimulated with a Dq, Lq, or Ld gene transfectant showed strong crossreactions with the other transfectants as targets, suggesting that the products of these genes are also functionally related. Thus, these studies suggest that the L molecule represents a prototypic structure shared by several D region gene products, and furthermore, that duplication of an Ld-like progenitor gene resulted in two Dq region class I genes, Dq and Lq. Unexpectedly, the sequences determined for the Dq and Lq genes are nearly identical to the sequences of two genes, A166 and A149, respectively, which were reported to encode the tumor-specific antigens; these novel class I genes were isolated from an H-2k fibrosarcoma, 1591. This raises the distinct possibility that these purported tumor-specific class I genes were introduced into this tumor by contamination.

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     (FILE 'HOME' ENTERED AT 07:13:43 ON 03 JUN 2002)

     FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 07:13:57 ON 03 JUN 2002
L1          127 S ZAUDERER M?/AU
L2            4 S L1 AND CTL?
L3            4 DUP REM L2 (0 DUPLICATES REMOVED)
L4       192122 S LIBRAR?
L5          366 S L4 (P) CTL
L6          146 S L5 AND PD<19970922
L7           89 S L6 (P) (EPITOP? OR PEPTID?)
L8           39 S L7 AND MHC

=> s l8 and (poxvirus or vaccinia)
L9            3 L8 AND (POXVIRUS OR VACCINIA)

=> dis l8 1-2 ibib abs

L8   ANSWER 1 OF 39  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:        1997:462415  CAPLUS
DOCUMENT NUMBER:         127:189254
TITLE:                   Antigen processing by proteasomes: insights into the
                         molecular basis of crypticity
AUTHOR(S):               Djaballah, Hakim
CORPORATE SOURCE:        MRC Transplantation Biology Group, Royal Postgraduate
                         Medical School, Hammersmith Hospital, London, W12 0NN,
                         UK
SOURCE:                  Mol. Biol. Rep. (1997), 24(1-2), 63-67
                         CODEN: MLBRBU; ISSN: 0301-4851
PUBLISHER:               Kluwer
DOCUMENT TYPE:           Journal; General Review
LANGUAGE:                English
AB   A review with 44 refs.  Eight to eleven amino acid residues are the sizes
     of predominant peptides found to be assocd. with MHC
     class I mols.  Proteasomes have been implicated in antigen processing and
     generation of such peptides.  Advanced methodologies in
     peptide elution together with sequence detn. have led to the
     characterization of MHC class I binding motifs.  More recently,
     screening of random peptide phage display libraries
     and synthetic combinatorial peptide libraries have
     also been successfully used.  This has led to the development and use of
     predictive algorithms to screen antigens for potential cytotoxic
     T-lymphocyte (CTL) epitopes.  Not all predicted
     epitopes will be generated in vivo and the emerging picture
     suggests differential presentation of predicted CTL
     epitopes ranging from cryptic to immunodominant.  Antigen
     processing by proteasomes is discussed, a hypothesis that the mol. basis
     of immunogenicity can be a function of proteasomal processing is advanced.
     This may explain how pathogens and tumors are able to escape
     immunosurveillance by altering sequences required by proteasomes for
     epitope generation.

L8   ANSWER 2 OF 39  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:        1997:147340  CAPLUS
DOCUMENT NUMBER:         126:198410
TITLE:                   Cytotoxic T cell induction with ratchet
                         peptide libraries
AUTHOR(S):               Kuebler, Peter J.; Nixon, Douglas F.
CORPORATE SOURCE:        United Biomedical, Inc., Hauppauge, NY, 11788, USA
SOURCE:                  Vaccine (1996), 14(17/18), 1664-1670
                         CODEN: VACCDE; ISSN: 0264-410X
PUBLISHER:               Elsevier
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB   Immunization with synthetic peptides are used to induce
     cytotoxic T cell (CTL) responses in vivo.  However, CTL
     peptide vaccines require the use of multiple peptides to
     overcome genetic diversity assocd. with MHC restriction, and
     prior epitope identification from the chosen protein template.
     The authors describe here a method whereby all nonamer sequences from a
     longer template can be synthesized simultaneously in a ratchet
     peptide library (RPL) covering all potential
     epitopes within a protein.  The authors synthesized an RPL based
     on a template sequence from the Plasmodium berghei circumsporozoite (CS)
     protein (CSRPL).  Using a lipopeptide formulation the authors immunized
     mice i.p. with the CSRPL and elicited CS specific CTL, which
     recognized the CS252-260 H-2Kd restricted CTL epitope.
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=> dis l8 3 ibib abs

L8   ANSWER 3 OF 39  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:        1997:111450  CAPLUS
DOCUMENT NUMBER:         126:184804
TITLE:                   Identification of tyrosinase-related protein 2 as a
                         tumor rejection antigen for the B16 melanoma
AUTHOR(S):               bloom, Matthew b.; Perry-Lalley, Donna; Robbins, Paul
                         F.; Li, Yong; El-Gamil, Mona; Rosenberg, Steven A.;
                         Yang, James C.
CORPORATE SOURCE:        Natl. Cancer Inst., Natl. Inst. Health, Bethesda, MD,
                         20892, USA
SOURCE:                  J. Exp. Med. (1997), 185(3), 453-459
                         CODEN: JEMEAV; ISSN: 0022-1007
PUBLISHER:               Rockefeller University Press
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB   Recently, major advances have been made in the identification of antigens
     from human melanoma which are recognized by T cells.  In spite of this,
     little is known about the optimal ways to use these antigens to treat
     patients with cancer, Progress in this area is likely to require accurate
     preclin. animal models, but the availability of such models has lagged
     behind developments in human tumor immunol.  Whereas many of the
     identified human melanoma antigens are normal tissue differentiation
     proteins, analogous murine tumor antigens have not yet been identified.
     In this paper we identify a normal tissue differentiation antigen,
     tyrosinase-related protein 2 (TRP-2), expressed by the murine B16 melanoma
     which was found by screening a cDNA library from B16 with
     tumor-reactive cytotoxic T lymphocytes (CTL).  A peptide
     conforming to the predicted MHC class I H2-Kb binding motif,
     TRP-2181-188, was identified a the major reactive epitope within
     TRP-2 recognized by these anti-B16 CTLs.  By site-directed
     mutagenesis, it was shown that alteration of this epitope
     eliminated recognition of TRP-2.  It was further demonstrated that the
     CTL line obtained from splenocytes by repeated stimulation in
     vitro with this peptide could recognize B16 tumor and was
     therapeutic against 3-d-old established pulmonary metastases.  The use of
     TRP-2 in a preclin. model of tumor immunotherapy may be helpful in
     suggesting optimal vaccination strategies for cancer therapy in patients.


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     FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 07:13:57 ON 03 JUN 2002
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L2             4 S L1 AND CTL?
L3             4 DUP REM L2 (0 DUPLICATES REMOVED)
L4        192122 S LIBRAR?
L5           366 S L4 (P) CTL
L6           146 S L5 AND PD<19970922
L7            89 S L6 (P) (EPITOP? OR PEPTID?)
L8            39 S L7 AND MHC
L9             3 S L8 AND (POXVIRUS OR VACCINIA)

=> s l7 and helper
L10            0 L7 AND HELPER

=> s l7 and tk
L11            0 L7 AND TK

=> s l7 and thymidine
L12            0 L7 AND THYMIDINE

=> s l7 and kinase
L13            0 L7 AND KINASE

=> s v7.5/tk
'TK' IS NOT A VALID FIELD CODE
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'TK' IS NOT A VALID FIELD CODE
L14            0 V7.5/TK

=> s v7.5 (1N) tk
L15            0 V7.5 (1N) TK

=> s l7 and homologous
L16           12 L7 AND HOMOLOGOUS

=> s l7 and (homologous (1N) recombination)
L17            0 L7 AND (HOMOLOGOUS (1N) RECOMBINATION)

=> s l7 and transfer (1N) plasmid)
UNMATCHED RIGHT PARENTHESIS 'PLASMID)'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s l7 and (transfer (1N) plasmid)
L18            0 L7 AND (TRANSFER (1N) PLASMID)

=> s (transfer (1N) plasmid)
L19         5607 (TRANSFER (1N) PLASMID)

=> dis his

     (FILE 'HOME' ENTERED AT 07:13:43 ON 03 JUN 2002)

     FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 07:13:57 ON 03 JUN 2002
L1           127 S ZAUDERER M?/AU
L2             4 S L1 AND CTL?
L3             4 DUP REM L2 (0 DUPLICATES REMOVED)
L4        192122 S LIBRAR?
L5           366 S L4 (P) CTL
L6           146 S L5 AND PD<19970922
L7            89 S L6 (P) (EPITOP? OR PEPTID?)
L8            39 S L7 AND MHC
L9             3 S L8 AND (POXVIRUS OR VACCINIA)
L10            0 S L7 AND HELPER
L11            0 S L7 AND TK
L12            0 S L7 AND THYMIDINE
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L13            0 S L7 AND KINASE
L14            0 S V7.5/TK
L15            0 S V7.5 (1N) TK
L16           12 S L7 AND HOMOLOGOUS
L17            0 S L7 AND (HOMOLOGOUS (1N) RECOMBINATION)
L18            0 S L7 AND (TRANSFER (1N) PLASMID)
L19         5607 S (TRANSFER (1N) PLASMID)

=> end
ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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